RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/644,084A

Source: 1Fw16

Date Processed by STIC: 12/28/06

ENTERED

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RAW SEQUENCE LISTING                    DATE: 12/28/2006
PATENT APPLICATION:  US/10/644,084A     TIME: 18:31:08

         Input Set : A:\2144.0100000_E1-X0202-USsq.txt
         Output Set: N:\CRF4\12282006\J644084A.raw
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 3 <110> APPLICANT: EISAI CO., LTD.
 5 <120> TITLE OF INVENTION: ADIP PROTEIN AND USE THEREOF
 7 <130> FILE REFERENCE: 2144.0100000
 9 <140> CURRENT APPLICATION NUMBER: US 10/644,084A
10 <141> CURRENT FILING DATE: 2003-08-20
12 <150> PRIOR APPLICATION NUMBER: JP 2002-284263
13 <151> PRIOR FILING DATE: 2002-09-27
15 <160> NUMBER OF SEQ ID NOS: 9
17 <170> SOFTWARE: PatentIn version 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2692
21 <212> TYPE: DNA
22 <213> ORGANISM: Mus musculus
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (80)..(1927)
28 <223> OTHER INFORMATION: /note="afadin-and alpha-actinin-binding protein"
30 <400> SEQUENCE: 1
31 cgtaggagag tgacaggagc tgttgtaagc gtcgcagcac tgagccgcct cctcaggtat    60
33 cctggctctg gaacttgct atg gga gat tgg atg act gtg aca gat cca gtt   112
34                     Met Gly Asp Trp Met Thr Val Thr Asp Pro Val
35                      1               5                  10
37 ctg tgt aca gaa aac aaa aat ctc tct caa tat acc tca gaa aca aag   160
38 Leu Cys Thr Glu Asn Lys Asn Leu Ser Gln Tyr Thr Ser Glu Thr Lys
39            15              20                  25
41 atg tct ccg tcc agt ttg tac tcc cag caa gtt ctg tgc tct tca gta   208
42 Met Ser Pro Ser Ser Leu Tyr Ser Gln Gln Val Leu Cys Ser Ser Val
43        30              35                  40
45 cct tta tcc aaa aac gtg cat ggt gtt ttc ggt gtc ttc tgc aca gga   256
46 Pro Leu Ser Lys Asn Val His Gly Val Phe Gly Val Phe Cys Thr Gly
47    45              50                  55
49 gag aac att gaa caa agt att tcc tat ctt gat cag gag ctg acc acc   304
50 Glu Asn Ile Glu Gln Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr
51 60              65                  70                  75
53 ttc ggg ttt cct tcc ttg tat gaa gaa tcc aaa agt aaa gag gca aag   352
54 Phe Gly Phe Pro Ser Leu Tyr Glu Glu Ser Lys Ser Lys Glu Ala Lys
55                80                  85                  90
57 aga gaa tta aat ata gtc gct gtt ctg aac tgt atg aac gag ctg ctc   400
58 Arg Glu Leu Asn Ile Val Ala Val Leu Asn Cys Met Asn Glu Leu Leu
59            95                  100                 105
61 gtg ctt cag cgg aag aac ctg ctg gcc cag gag agc gtg gag aca cag   448
62 Val Leu Gln Arg Lys Asn Leu Leu Ala Gln Glu Ser Val Glu Thr Gln
63        110                 115                 120
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65 aac ttg aag ctg ggc agt gac atg gac cac ctg cag agc tgc tac gcc      496
66 Asn Leu Lys Leu Gly Ser Asp Met Asp His Leu Gln Ser Cys Tyr Ala
67     125             130             135
69 aaa ctt aag gag cag ttg gaa acg tcc agg cgg gag atg atc ggg ctt      544
70 Lys Leu Lys Glu Gln Leu Glu Thr Ser Arg Arg Glu Met Ile Gly Leu
71 140             145             150             155
73 caa gag aga gac agg cag ctg cag tgc aag aac agg agt ttg cat cag      592
74 Gln Glu Arg Asp Arg Gln Leu Gln Cys Lys Asn Arg Ser Leu His Gln
75             160             165             170
77 ctc ctg aag aat gag aaa gat gag gta caa aaa tta caa aat atc ata      640
78 Leu Leu Lys Asn Glu Lys Asp Glu Val Gln Lys Leu Gln Asn Ile Ile
79             175             180             185
81 gcc agc cgg gct act cag tat aat cat gat gtg aag agg aag gag cgt      688
82 Ala Ser Arg Ala Thr Gln Tyr Asn His Asp Val Lys Arg Lys Glu Arg
83             190             195             200
85 gaa tat aat aag cta aag gag cgc ctg cat cag ctc gtt atg aac aag      736
86 Glu Tyr Asn Lys Leu Lys Glu Arg Leu His Gln Leu Val Met Asn Lys
87     205             210             215
89 aag gat aaa aac ata gcc atg gat gtt tta aat tat gtg ggt cga gct      784
90 Lys Asp Lys Asn Ile Ala Met Asp Val Leu Asn Tyr Val Gly Arg Ala
91 220             225             230             235
93 gat ggc aaa cga ggc tca tgg agg act gac aaa aca gaa gcc agg aat      832
94 Asp Gly Lys Arg Gly Ser Trp Arg Thr Asp Lys Thr Glu Ala Arg Asn
95             240             245             250
97 gaa gat gag atg tac aaa att ctg ttg aat gat tat gag tac cgc cag      880
98 Glu Asp Glu Met Tyr Lys Ile Leu Leu Asn Asp Tyr Glu Tyr Arg Gln
99             255             260             265
101 aag cag atc ctg atg gag aac gcg gag ctg aag aag gtc ctc cag cag      928
102 Lys Gln Ile Leu Met Glu Asn Ala Glu Leu Lys Lys Val Leu Gln Gln
103             270             275             280
105 atg aag aag gag atg atc tct ctc ctg tct cct cag aag aag aag ccc      976
106 Met Lys Lys Glu Met Ile Ser Leu Leu Ser Pro Gln Lys Lys Lys Pro
107     285             290             295
109 agg gaa aga gca gag gac ggc aca ggc act gtt gct atc tcc gat ata      1024
110 Arg Glu Arg Ala Glu Asp Gly Thr Gly Thr Val Ala Ile Ser Asp Ile
111 300             305             310             315
113 gaa gat gac tct ggg gaa ctg agc aga gac agc gtg tgg ggc ctt tcc      1072
114 Glu Asp Asp Ser Gly Glu Leu Ser Arg Asp Ser Val Trp Gly Leu Ser
115             320             325             330
117 tgt gac act gtg aga gag cag ctg aca aac agc atc agg aaa cag tgg      1120
118 Cys Asp Thr Val Arg Glu Gln Leu Thr Asn Ser Ile Arg Lys Gln Trp
119             335             340             345
121 aga att ttg aaa agt cat gta gaa aaa ctc gat aac caa gct tcg aag      1168
122 Arg Ile Leu Lys Ser His Val Glu Lys Leu Asp Asn Gln Ala Ser Lys
123             350             355             360
125 gta cac tca gag ggc ctt aat gag gag gac gtc atc tca cga caa gac      1216
126 Val His Ser Glu Gly Leu Asn Glu Glu Asp Val Ile Ser Arg Gln Asp
127     365             370             375
129 cat gag caa gag act gag aaa ctg gag ctg gag att gag cgg tgt aaa      1264
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Input Set : A:\2144.0100000_E1-X0202-USsq.txt
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130 His Glu Gln Glu Thr Glu Lys Leu Glu Leu Glu Ile Glu Arg Cys Lys
131 380                 385                 390                 395
133 gag atg atc aag gct cag cag cag ctc tta cag cag cag ctg gcc acc    1312
134 Glu Met Ile Lys Ala Gln Gln Gln Leu Leu Gln Gln Gln Leu Ala Thr
135                 400                 405                 410
137 acg tgt gat gat gac acc acc tca ctg ttg cga gac tgt tac ttg ctg    1360
138 Thr Cys Asp Asp Asp Thr Thr Ser Leu Leu Arg Asp Cys Tyr Leu Leu
139                 415                 420                 425
141 gaa gaa aag gaa cgc ctt aaa gaa gag tgg acc ctt ttt aaa gag caa    1408
142 Glu Glu Lys Glu Arg Leu Lys Glu Glu Trp Thr Leu Phe Lys Glu Gln
143         430                 435                 440
145 aaa aag aat ttt gag aga gaa agg cga agc ttt aca gaa gct gcc att    1456
146 Lys Lys Asn Phe Glu Arg Glu Arg Arg Ser Phe Thr Glu Ala Ala Ile
147     445                 450                 455
149 cga ttg ggg ttg gag aga aag gcg ttt gaa gaa gag cga gcc agc tgg    1504
150 Arg Leu Gly Leu Glu Arg Lys Ala Phe Glu Glu Glu Arg Ala Ser Trp
151 460                 465                 470                 475
153 gta aag cag cag ttt tta aac atg acg aac ttt gac cac cag aac tca    1552
154 Val Lys Gln Gln Phe Leu Asn Met Thr Asn Phe Asp His Gln Asn Ser
155                 480                 485                 490
157 gaa aat gtg aaa ctt ttc agt gcc ttc tca gga agt tct gat cca gac    1600
158 Glu Asn Val Lys Leu Phe Ser Ala Phe Ser Gly Ser Ser Asp Pro Asp
159                 495                 500                 505
161 aat ctt ata gtc cac tca cgg cca cgg caa aag aag cta cac agt gtg    1648
162 Asn Leu Ile Val His Ser Arg Pro Arg Gln Lys Lys Leu His Ser Val
163         510                 515                 520
165 gct aat ggg gtg cca gct tgc aca tca aaa ctg act aaa tct ctt cct    1696
166 Ala Asn Gly Val Pro Ala Cys Thr Ser Lys Leu Thr Lys Ser Leu Pro
167     525                 530                 535
169 gcc tca cct tct act tca gac ttt cgc cag aca cat tca tgt gtg tct    1744
170 Ala Ser Pro Ser Thr Ser Asp Phe Arg Gln Thr His Ser Cys Val Ser
171 540                 545                 550                 555
173 gaa cac agt tcc atc agt gtg ctg aat ata act cct gaa gaa agt aaa    1792
174 Glu His Ser Ser Ile Ser Val Leu Asn Ile Thr Pro Glu Glu Ser Lys
175                 560                 565                 570
177 cca agt gag gtt gca aga gaa agc acg gat cag aag tgg agc gtg cag    1840
178 Pro Ser Glu Val Ala Arg Glu Ser Thr Asp Gln Lys Trp Ser Val Gln
179                 575                 580                 585
181 tcg agg ccc agc tcg cgg gag ggg tgc tac agc gga tgc tcc tcg gcc    1888
182 Ser Arg Pro Ser Ser Arg Glu Gly Cys Tyr Ser Gly Cys Ser Ser Ala
183         590                 595                 600
185 ttc agg agc gct cac ggg gac cga gat gac tta cct taa atgtgcgggc     1937
186 Phe Arg Ser Ala His Gly Asp Arg Asp Asp Leu Pro
187     605                 610                 615
189 tgcagtgctg ttcccagatg tgcgctagag gagttgacac agggtgtagc ataaagtcag   1997
191 tcgtctaact taagatgctc agagttgttt gtttggactt cgctgtcttc ccccaaagag   2057
193 ctgaaatgct aagctactta aaaggatgca aagctttggt tgtgtgttag taacagaagc   2117
195 ccctggctct gtgactgcag gaatgcatgg cgtttggatg gaaacagaag cgctggaatg   2177
197 attgcctcgc caggtaccga gaagagcact tttagggact ggttcctgta aacattaaat   2237
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RAW SEQUENCE LISTING   DATE: 12/28/2006
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Input Set : A:\2144.0100000_E1-X0202-USsq.txt
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199 attcgtccca agtgtggttg gcattggaag tgtagccttt acttgaatgt atactgtaga  2297
201 tttttaacaa agcaggttct atatttatta tgtttagtgt gattttggga ttacctcttt  2357
203 catatgtttt gtgtctgtac ataaatatac atgactatgt taagaggctt taaggtttaa  2417
205 aaacttcaca ccatgcttga gtatagcatt tcatgccaat taaaatgttt tcagtggcat  2477
207 ggtgtttaca gaggttagga ccactgccac atgacagtta agactttatt tttaagccat  2537
209 ctgggcaata aaaattcaaa gccccttcat aagctgagtt cagataacta gaactactaa  2597
211 cgttacattt ttgagatttt taaagcattg tattttattt tatatatgtg aatgttataa  2657
213 tttctaagag gaatattgat tatggagtaa tgggg  2692
216 <210> SEQ ID NO: 2
217 <211> LENGTH: 615
218 <212> TYPE: PRT
219 <213> ORGANISM: Mus musculus
221 <400> SEQUENCE: 2
223 Met Gly Asp Trp Met Thr Val Thr Asp Pro Val Leu Cys Thr Glu Asn
224 1               5                   10                  15
227 Lys Asn Leu Ser Gln Tyr Thr Ser Glu Thr Lys Met Ser Pro Ser Ser
228             20                  25                  30
231 Leu Tyr Ser Gln Gln Val Leu Cys Ser Ser Val Pro Leu Ser Lys Asn
232         35                  40                  45
235 Val His Gly Val Phe Gly Val Phe Cys Thr Gly Glu Asn Ile Glu Gln
236     50                  55                  60
239 Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr Phe Gly Phe Pro Ser
240 65                  70                  75                  80
243 Leu Tyr Glu Glu Ser Lys Ser Lys Glu Ala Lys Arg Glu Leu Asn Ile
244             85                  90                  95
247 Val Ala Val Leu Asn Cys Met Asn Glu Leu Leu Val Leu Gln Arg Lys
248             100                 105                 110
251 Asn Leu Leu Ala Gln Glu Ser Val Glu Thr Gln Asn Leu Lys Leu Gly
252         115                 120                 125
255 Ser Asp Met Asp His Leu Gln Ser Cys Tyr Ala Lys Leu Lys Glu Gln
256     130                 135                 140
259 Leu Glu Thr Ser Arg Arg Glu Met Ile Gly Leu Gln Glu Arg Asp Arg
260 145                 150                 155                 160
263 Gln Leu Gln Cys Lys Asn Arg Ser Leu His Gln Leu Leu Lys Asn Glu
264             165                 170                 175
267 Lys Asp Glu Val Gln Lys Leu Gln Asn Ile Ile Ala Ser Arg Ala Thr
268             180                 185                 190
271 Gln Tyr Asn His Asp Val Lys Arg Lys Glu Arg Glu Tyr Asn Lys Leu
272         195                 200                 205
275 Lys Glu Arg Leu His Gln Leu Val Met Asn Lys Lys Asp Lys Asn Ile
276     210                 215                 220
279 Ala Met Asp Val Leu Asn Tyr Val Gly Arg Ala Asp Gly Lys Arg Gly
280 225                 230                 235                 240
283 Ser Trp Arg Thr Asp Lys Thr Glu Ala Arg Asn Glu Asp Glu Met Tyr
284             245                 250                 255
287 Lys Ile Leu Leu Asn Asp Tyr Glu Tyr Arg Gln Lys Gln Ile Leu Met
288             260                 265                 270
291 Glu Asn Ala Glu Leu Lys Lys Val Leu Gln Gln Met Lys Lys Glu Met
292         275                 280                 285
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295 Ile Ser Leu Leu Ser Pro Gln Lys Lys Lys Pro Arg Glu Arg Ala Glu
296     290                 295                 300
299 Asp Gly Thr Gly Thr Val Ala Ile Ser Asp Ile Glu Asp Asp Ser Gly
300 305                 310                 315                 320
303 Glu Leu Ser Arg Asp Ser Val Trp Gly Leu Ser Cys Asp Thr Val Arg
304                 325                 330                 335
307 Glu Gln Leu Thr Asn Ser Ile Arg Lys Gln Trp Arg Ile Leu Lys Ser
308                 340                 345                 350
311 His Val Glu Lys Leu Asp Asn Gln Ala Ser Lys Val His Ser Glu Gly
312         355                 360                 365
315 Leu Asn Glu Glu Asp Val Ile Ser Arg Gln Asp His Glu Gln Glu Thr
316     370                 375                 380
319 Glu Lys Leu Glu Leu Glu Ile Glu Arg Cys Lys Glu Met Ile Lys Ala
320 385                 390                 395                 400
323 Gln Gln Gln Leu Leu Gln Gln Gln Leu Ala Thr Thr Cys Asp Asp Asp
324                 405                 410                 415
327 Thr Thr Ser Leu Leu Arg Asp Cys Tyr Leu Leu Glu Glu Lys Glu Arg
328                 420                 425                 430
331 Leu Lys Glu Glu Trp Thr Leu Phe Lys Glu Gln Lys Lys Asn Phe Glu
332         435                 440                 445
335 Arg Glu Arg Arg Ser Phe Thr Glu Ala Ala Ile Arg Leu Gly Leu Glu
336     450                 455                 460
339 Arg Lys Ala Phe Glu Glu Glu Arg Ala Ser Trp Val Lys Gln Gln Phe
340 465                 470                 475                 480
343 Leu Asn Met Thr Asn Phe Asp His Gln Asn Ser Glu Asn Val Lys Leu
344                 485                 490                 495
347 Phe Ser Ala Phe Ser Gly Ser Ser Asp Pro Asp Asn Leu Ile Val His
348                 500                 505                 510
351 Ser Arg Pro Arg Gln Lys Lys Leu His Ser Val Ala Asn Gly Val Pro
352         515                 520                 525
355 Ala Cys Thr Ser Lys Leu Thr Lys Ser Leu Pro Ala Ser Pro Ser Thr
356     530                 535                 540
359 Ser Asp Phe Arg Gln Thr His Ser Cys Val Ser Glu His Ser Ser Ile
360 545                 550                 555                 560
363 Ser Val Leu Asn Ile Thr Pro Glu Glu Ser Lys Pro Ser Glu Val Ala
364                 565                 570                 575
367 Arg Glu Ser Thr Asp Gln Lys Trp Ser Val Gln Ser Arg Pro Ser Ser
368                 580                 585                 590
371 Arg Glu Gly Cys Tyr Ser Gly Cys Ser Ser Ala Phe Arg Ser Ala His
372         595                 600                 605
375 Gly Asp Arg Asp Asp Leu Pro
376     610                 615
379 <210> SEQ ID NO: 3
380 <211> LENGTH: 3195
381 <212> TYPE: DNA
382 <213> ORGANISM: Rattus norvegicus
385 <220> FEATURE:
386 <221> NAME/KEY: CDS
387 <222> LOCATION: (79)..(1920)
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/28/2006
PATENT APPLICATION: US/10/644,084A   TIME: 18:31:09

Input Set : A:\2144.0100000_E1-X0202-USsq.txt
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the
<220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 2422

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8

VERIFICATION SUMMARY   DATE: 12/28/2006
PATENT APPLICATION: **US/10/644,084A**   TIME: 18:31:09

Input Set : **A:\2144.0100000_E1-X0202-USsq.txt**
Output Set: **N:\CRF4\12282006\J644084A.raw**

L:569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2420